1646

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/517,256_

Source: _PCT_

Date Processed by STIC: _1/31/06_

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PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
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2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
    U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/517,256_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ✓ Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 ____ Invalid Line Length
The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino Numbering
The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

4 ✓ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 ____ Variable Length
Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please insert the following lines for **each** skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 ____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

10 ____ Invalid <213> Response
Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence

11 ____ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____ PatentIn 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa
"n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – Biotechnology Systems Branch – 09/09/2003

PCT

RAW SEQUENCE LISTING   DATE: 01/31/2006
PATENT APPLICATION: **US/10/517,256**   TIME: 15:47:22

Input Set : **N:\SMITH\PTO.TS.txt**   *see item 4 on Err*
Output Set: **N:\CRF4\01312006\J517256.raw**   *Summary Sheet*

```
   3 <110> APPLICANT: Scott, Kieran
   5 <120> TITLE OF INVENTION: Method of inhibiting prostate cancer cell proliferation
   7 <130> FILE REFERENCE: 501543
C-->  9 <140> CURRENT APPLICATION NUMBER: US/10/517,256
C-->  9 <141> CURRENT FILING DATE: 2004-12-07
   9 <150> PRIOR APPLICATION NUMBER: PS2826
  10 <151> PRIOR FILING DATE: 2002-06-07
  12 <160> NUMBER OF SEQ ID NOS: 4
  14 <170> SOFTWARE: PatentIn version 3.1
```

pp 1-4, 6

ERRORED SEQUENCES

Does Not Comply
Corrected Diskette Needed

```
  16 <210> SEQ ID NO: 1
  17 <211> LENGTH: 997
  18 <212> TYPE: DNA
  19 <213> ORGANISM: Homo sapiens
  21 <400> SEQUENCE: 1
```

see item 1
on Err Summary Sheet

```
E-->  22 gaaggaaaaa gagcaacaga tccagggagc attcacctgc cctgtctcca aacagccttg →  60
      23  60
E-->  25 tgcctcacct acccccaacc tcccagaggg agcagctatt taaggggagc aggagtgcag → 120
      26 120
E-->  28 aacaaacaag acggcctggg gatacaactc tggagtcctc tgagagagcc accaaggagg → 180
      29 180
E-->  31 agcaggggag cgacggccgg ggcagaagtt gagaccaccc agcagaggag ctaggccagt
      32 240
E-->  34 ccatctgcat ttgtcacccc agaactctta ccatgaagac cctcctactg ttggcagtga
      35 300
E-->  37 tcatgatctt tggcctactg caggcccatg ggaatttggt gaatttccac agaatgatca
      38 360
E-->  40 agttgacgac aggaaaggaa gccgcactca gttatggctt ctacggctgc cactgtggcg
      41 420
E-->  43 tgggtggcag aggatccccc aaggatgcaa cggatcgctg ctgtgtcact catgactgtt
      44 480
E-->  46 gctacaaacg tctggagaaa cgtggatgtg gcaccaaatt tctgagctac aagtttagca
      47 540
E-->  49 actcggggag cagaatcacc tgtgcaaaac aggactcctg cagaagtcaa ctgtgtgagt
      50 600
E-->  52 gtgataaggc tgctgccacc tgttttgcta gaaacaagac gacctacaat aaaaagtacc
      53 660
E-->  55 agtactattc caataaacac tgcagaggga gcacccctcg ttgctgagtc ccctcttccc
      56 720
E-->  58 tggaaacctt ccacccagtg ctgaatttcc ctctctcata ccctccctcc ctaccctaac
```

RAW SEQUENCE LISTING   DATE: 01/31/2006
PATENT APPLICATION: US/10/517,256   TIME: 15:47:22

Input Set : **N:\SMITH\PTO.TS.txt**
Output Set: **N:\CRF4\01312006\J517256.raw**

```
      59 780
E--> 61 caagttcctt ggccatgcag aaagcatccc tcacccatcc tagaggccag gcaggagccc
      62 840
E--> 64 ttctataccc acccagaatg agacatccag cagatttcca gccttctact gctctcctcc
      65 900
E--> 67 acctcaactc cgtgcttaac caaagaagct gtactccggg gggtctcttc tgaataaagc
      68 960
E--> 70 aattagcaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa
      71 997
      74 <210> SEQ ID NO: 2
      75 <211> LENGTH: 2875
      76 <212> TYPE: DNA
      77 <213> ORGANISM: Homo sapiens
      79 <400> SEQUENCE: 2
E--> 80 gaattctccg gagctgaaaa aggatcctga ctgaaagcta gaggcattga ggagcctgaa
      81 60
E--> 83 gattctcagg ttttaaagac gctagagtgc caaagaagac tttgaagtgt gaaaacattt
      84 120
E--> 86 cctgtaattg aaaccaaaat gtcatttata gatccttacc agcacattat agtggagcac
      87 180
E--> 89 cagtattccc acaagtttac ggtagtggtg ttacgtgcca ccaaagtgac aaaggggggcc
      90 240
E--> 92 tttggtgaca tgcttgatac tccagatccc tatgtggaac tttttatctc tacaacccct
      93 300
E--> 95 gacagcagga agagaacaag acatttcaat aatgacataa accctgtgtg gaatgagacc
      96 360
E--> 98 tttgaattta ttttggatcc taatcaggaa aatgttttgg agattacgtt aatggatgcc
      99 420
E--> 101 aattatgtca tggatgaaac tctagggaca gcaacattta ctgtatcttc tatgaaggtg
      102 480
E--> 104 ggagaaaaga aagaagttcc ttttattttc aaccaagtca ctgaaatggt tctagaaatg
      105 540
E--> 107 tctcttgaag tttgctcatg cccagaccta cgatttagta tggctctgtg tgatcaggag
      108 600
E--> 110 aagactttca gacaacagag aaaagaacac ataagggaga gcatgaagaa actcttgggt
      111 660
E--> 113 ccaaagaata gtgaaggatt gcattctgca cgtgatgtgc ctgtggtagc catattgggt
      114 720
E--> 116 tcaggtgggg gtttccgagc catggtggga ttctctggtg tgatgaaggc attatacgaa
      117 780
E--> 119 tcaggaattc tggattgtgc tacctacgtt gctggtcttt ctggctccac ctggtatatg
      120 840
E--> 122 tcaaccttgt attctcaccc tgattttcca gagaaagggc cagaggagat taatgaagaa
      123 900
E--> 125 ctaatgaaaa atgttagcca caatcccctt ttacttctca caccacagaa agttaaaaga
      126 960
E--> 128 tatgttgagt ctttatggaa gaagaaaagc tctggacaac ctgtcacctt tactgacatc
      129 1020
E--> 131 tttgggatgt aataggagga aacactaatt cataatagaa tgaatactac tctgagcagt
```

```
        132 1080
E--> 134 ttgaaggaaa aagttaatac tgcacaatgc cctttacctc ttttcacctg tcttcatgtc
        135 1140
E--> 137 aaacctgacg tttcagagct gatgtttgca gattgggttg aatttagtcc atacgaaatt
        138 1200
E--> 140 ggcatggcta aatatggtac ttttatggct cccgacttat ttggaagcaa attttttatg
        141 1260
E--> 143 ggaacagtcg ttaagaagta tgaagaaaac cccttgcatt tcttaatggg tgtctggggc
        144 1320
E--> 146 agtgcctttt ccatattgtt caacagagtt ttgggcgttt ctggttcaca aagcagaggc
        147 1380
E--> 149 tccacaatgg aggaagaatt agaaaatatt accacaaagc atattgtgag taatgatagc
        150 1440
E--> 152 tcggacagtg atgatgaatc acacgaaccc aaaggcactg aaaatgaaga tgctggaagt
        153 1500
E--> 155 gactatcaaa gtgataatca agcaagttgg attcatcgta tgataatggc cttggtgagt
        156 1560
E--> 158 gattcagctt tattcaatac cagagaagga cgtgctggga aggtacacaa cttcatgctg
        159 1620
E--> 161 ggcttgaatc tcaatacatc ttatccactg tctcctttga gtgactttgc cacacaggac
        162 1680
E--> 164 tcctttgatg atgatgaact ggatgcagct gtagcagatc ctgatgaatt tgagcgaata
        165 1740
E--> 167 tatgagcctc tggatgtcaa aagtaaaaag attcatgtag tggacagtgg gctcacattt
        168 1800
E--> 170 aacctgccgt atcccttgat actgagacct cagagagggg ttgatctcat aatctccttt
        171 1860
E--> 173 gacttttctg caaggccaag tgactctagt cctccgttca aggaacttct acttgcagaa
        174 1920
E--> 176 aagtgggcta aaatgaacaa gctccccttt ccaaagattg atccttatgt gtttgatcgg
        177 1980
E--> 179 gaagggctga aggagtgcta tgtctttaaa cccaagaatc ctgatatgga gaaagattgc
        180 2040
E--> 182 ccaaccatca tccactttgt tctggccaac atcaacttca gaaagtacaa ggctccaggt
        183 2100
E--> 185 gttccaaggg aaactgagga agagaaagaa atcgctgact ttgatatttt tgatgaccca
        186 2160
E--> 188 gaatcaccat tttcaacctt caattttcaa tatccaaatc aagcattcaa aagactacat
        189 2220
E--> 191 gatcttatgc acttcaatac tctgaacaac attgatgtga taaaagaagc catggttgaa
        192 2280
E--> 194 agcattgaat atagaagaca gaatccatct cgttgctctg tttcccttag taatgttgag
        195 2340
E--> 197 gcaagaagat ttttcaacaa ggagtttcta agtaaaccca agcatagtt catgtactgg
        198 2400
E--> 200 aaatggcagc agtttctgat gctgaggcag tttgcaatcc catgacaact ggatttaaaa
        201 2460
E--> 203 gtacagtaca gatagtcgta ctgatcatga gagactggct gatactcaaa gttgcagtta
        204 2520
```

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PATENT APPLICATION: US/10/517,256   TIME: 15:47:22

Input Set : N:\SMITH\PTO.TS.txt
Output Set: N:\CRF4\01312006\J517256.raw

E--> 206 cttagctgca tgagaataat actattataa gttaggtgac aaatgatgtt gattatgtaa
      207 2580
E--> 209 ggatatactt agctacattt tcagtcagta tgaacttcct gatacaaatg tagggatata
      210 2640
E--> 212 tactgtattt ttaaacattt ctcaccaact ttcttatgtg tgttcttttt aaaaattttt
      213 2700
E--> 215 tttcttttaa aatatttaac agttcaatct caataagacc tcgcattatg tatgaatgtt
      216 2760
E--> 218 attcactgac tagatttatt cataccatga gacaacacta tttttattta tatatgcata
      219 2820
E--> 221 tatatacata catgaaataa atacatcaat ataaaaataa aaaaaaacgg aattc
      222 2875
      268 <210> SEQ ID NO: 4
      269 <211> LENGTH: 749
      270 <212> TYPE: PRT
      271 <213> ORGANISM: Homo sapiens
      273 <400> SEQUENCE: 4
      275 Met Ser Phe Ile Asp Pro Tyr Gln His Ile Ile Val Glu His Gln Tyr
      276 1   5   10   15
      279 Ser His Lys Phe Thr Val Val Val Leu Arg Ala Thr Lys Val Thr Lys
      280   20   25   30
      283 Gly Ala Phe Gly Asp Met Leu Asp Thr Pro Asp Pro Tyr Val Glu Leu
      284   35   40   45
      287 Phe Ile Ser Thr Thr Pro Asp Ser Arg Lys Arg Thr Arg His Phe Asn
      288   50   55   60
      291 Asn Asp Ile Asn Pro Val Trp Asn Glu Thr Phe Glu Phe Ile Leu Asp
      292 65   70   75   80
      295 Pro Asn Gln Glu Asn Val Leu Glu Ile Thr Leu Met Asp Ala Asn Tyr
      296   85   90   95
      299 Val Met Asp Glu Thr Leu Gly Thr Ala Thr Phe Thr Val Ser Ser Met
      300   100   105   110
      303 Lys Val Gly Glu Lys Lys Glu Val Pro Phe Ile Phe Asn Gln Val Thr
      304   115   120   125
      307 Glu Met Val Leu Glu Met Ser Leu Glu Val Cys Ser Cys Pro Asp Leu
      308   130   135   140
      311 Arg Phe Ser Met Ala Leu Cys Asp Gln Glu Lys Thr Phe Arg Gln Gln
      312 145   150   155   160
      315 Arg Lys Glu His Ile Arg Glu Ser Met Lys Lys Leu Leu Gly Pro Lys
      316   165   170   175
      319 Asn Ser Glu Gly Leu His Ser Ala Arg Asp Val Pro Val Val Ala Ile
      320   180   185   190
      323 Leu Gly Ser Gly Gly Gly Phe Arg Ala Met Val Gly Phe Ser Gly Val
      324   195   200   205
      327 Met Lys Ala Leu Tyr Glu Ser Gly Ile Leu Asp Cys Ala Thr Tyr Val
      328   210   215   220
      331 Ala Gly Leu Ser Gly Ser Thr Trp Tyr Met Ser Thr Leu Tyr Ser His
      332 225   230   235   240
      335 Pro Asp Phe Pro Glu Lys Gly Pro Glu Glu Ile Asn Glu Glu Leu Met
      336   245   250   255

```
339 Lys Asn Val Ser His Asn Pro Leu Leu Leu Leu Thr Pro Gln Lys Val
340             260             265             270
343 Lys Arg Tyr Val Glu Ser Leu Trp Lys Lys Lys Ser Ser Gly Gln Pro
344             275             280             285
347 Val Thr Phe Thr Asp Ile Phe Gly Met Leu Ile Gly Glu Thr Leu Ile
348             290             295             300
351 His Asn Arg Met Asn Thr Thr Leu Ser Ser Leu Lys Glu Lys Val Asn
352 305             310             315             320
355 Thr Ala Gln Cys Pro Leu Pro Leu Phe Thr Cys Leu His Val Lys Pro
356             325             330             335
359 Asp Val Ser Glu Leu Met Phe Ala Asp Trp Val Glu Phe Ser Pro Tyr
360             340             345             350
363 Glu Ile Gly Met Ala Lys Tyr Gly Thr Phe Met Ala Pro Asp Leu Phe
364             355             360             365
367 Gly Ser Lys Phe Phe Met Gly Thr Val Val Lys Lys Tyr Glu Glu Asn
368             370             375             380
371 Pro Leu His Phe Leu Met Gly Val Trp Gly Ser Ala Phe Ser Ile Leu
372 385             390             395             400
375 Phe Asn Arg Val Leu Gly Val Ser Gly Ser Gln Ser Arg Gly Ser Thr
376             405             410             415
379 Met Glu Glu Glu Leu Glu Asn Ile Thr Thr Lys His Ile Val Ser Asn
380             420             425             430
383 Asp Ser Ser Asp Ser Asp Asp Glu Ser His Glu Pro Lys Gly Thr Glu
384             435             440             445
387 Asn Glu Asp Ala Gly Ser Asp Tyr Gln Ser Asp Asn Gln Ala Ser Trp
388             450             455             460
391 Ile His Arg Met Ile Met Ala Leu Val Ser Asp Ser Ala Leu Phe Asn
392 465             470             475             480
395 Thr Arg Glu Gly Arg Ala Gly Lys Val His Asn Phe Met Leu Gly Leu
396             485             490             495
399 Asn Leu Asn Thr Ser Tyr Pro Leu Ser Pro Leu Ser Asp Phe Ala Thr
400             500             505             510
403 Gln Asp Ser Phe Asp Asp Asp Glu Leu Asp Ala Ala Val Ala Asp Pro
404             515             520             525
407 Asp Glu Phe Glu Arg Ile Tyr Glu Pro Leu Asp Val Lys Ser Lys Lys
408             530             535             540
411 Ile His Val Val Asp Ser Gly Leu Thr Phe Asn Leu Pro Tyr Pro Leu
412 545             550             555             560
415 Ile Leu Arg Pro Gln Arg Gly Val Asp Leu Ile Ile Ser Phe Asp Phe
416             565             570             575
419 Ser Ala Arg Pro Ser Asp Ser Ser Pro Pro Phe Lys Glu Leu Leu Leu
420             580             585             590
423 Ala Glu Lys Trp Ala Lys Met Asn Lys Leu Pro Phe Pro Lys Ile Asp
424             595             600             605
427 Pro Tyr Val Phe Asp Arg Glu Gly Leu Lys Glu Cys Tyr Val Phe Lys
428             610             615             620
431 Pro Lys Asn Pro Asp Met Glu Lys Asp Cys Pro Thr Ile Ile His Phe
432 625             630             635             640
435 Val Leu Ala Asn Ile Asn Phe Arg Lys Tyr Lys Ala Pro Gly Val Pro
```

RAW SEQUENCE LISTING   DATE: 01/31/2006
PATENT APPLICATION: US/10/517,256   TIME: 15:47:22

Input Set : **N:\SMITH\PTO.TS.txt**
Output Set: **N:\CRF4\01312006\J517256.raw**

```
436                    645                650                655
439 Arg Glu Thr Glu Glu Glu Lys Glu Ile Ala Asp Phe Asp Ile Phe Asp
440                    660                665                670
443 Asp Pro Glu Ser Pro Phe Ser Thr Phe Asn Phe Gln Tyr Pro Asn Gln
444            675                680                685
447 Ala Phe Lys Arg Leu His Asp Leu Met His Phe Asn Thr Leu Asn Asn
448        690                695                700
451 Ile Asp Val Ile Lys Glu Ala Met Val Glu Ser Ile Glu Tyr Arg Arg
452 705                710                715                720
455 Gln Asn Pro Ser Arg Cys Ser Val Ser Leu Ser Asn Val Glu Ala Arg
456                    725                730                735
459 Arg Phe Phe Asn Lys Glu Phe Leu Ser Lys Pro Lys Ala
460                    740                745
E--> 471 9
```

VERIFICATION SUMMARY   DATE: 01/31/2006
PATENT APPLICATION: **US/10/517,256**   TIME: 15:47:23

Input Set : **N:\SMITH\PTO.TS.txt**
Output Set: **N:\CRF4\01312006\J517256.raw**

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:22 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:1
M:254 Repeated in SeqNo=1
L:80 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:60 SEQ:2
M:254 Repeated in SeqNo=2
L:471 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4